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SEQUENCE LISTING

<110> Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-27

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<150> US 60/154,652

<151> 1999-09-20

<160> 4

<170> PatentIn Ver. 2.0

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<211> 1907

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (101)..(1804)

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Met Gly Leu Phe His
1 5

cta act ctc ttt gga ctt tta ttg tgt agt ctt ccc att tct ctt gtt 163
Leu Thr Leu Phe Gly Leu Leu Leu Cys Ser Leu Pro Ile Ser Leu Val
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gct aaa ttc cct gag tct gta ggt cat aag atc ctt tat ata agt acg 211
Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile Leu Tyr Ile Ser Thr
25 30 35

caa tct aca cag cag gcc tta gca aca tat ctg gaa gct cta gat gcc 259
Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu Glu Ala Leu Asp Ala
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50 tac ggt gat cat gac ttc ttc gtt tta aga aaa atc gga gaa gac tat 307
Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys Ile Gly Glu Asp Tyr
55 60 65

ctc aag caa agc atc cac tcc tca gat ccg caa act aga aaa agc acc 355
Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln Thr Arg Lys Ser Thr
70 75 80 85

atc att gga gca ggc ctg gcg gga tct tca gaa gcc ttg gac gtg ctc 403
Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu Ala Leu Asp Val Leu
90 95 100

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	Arg	Leu	Ala	Asn	Leu	Lys	Asn	Thr	Lys	Val	Ile	Asp	His	Leu	His	Ser	
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	455 460 465	
	att tat aat ctc acc aaa gat cct gaa aaa aaa cgt tct ctc cat gat	1555
	Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys Arg Ser Leu His Asp	
	470 475 480 485	
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	535 540 545	
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	550 555 560 565	
	att gtg gag taacccaac ctacgtctta tgaaacgttg cttcttattt	1844
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 35 40 45
 20 Glu Ala Leu Asp Ala Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys
 50 55 60
 Ile Gly Glu Asp Tyr Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln
 65 70 75 80
 Thr Arg Lys Ser Thr Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu
 85 90 95
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 Gln Leu Leu Val Leu Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser
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 145 150 155 160
 40 Asp His Leu His Ser Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys
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 Leu Arg Asn Leu Leu Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile
 225 230 235 240
 Leu Tyr Ala Leu Gly Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile
 245 250 255
 60 Lys Lys Gln Leu Gln Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala
 260 265 270

Gln Ala Leu Ile Ala Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile
 275 280 285
 Lys Lys Gln Ala Leu Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg
 290 295 300
 His Leu Pro Ser Glu Ile Gly Ile Pro Ile Ala Leu Pro Ile Phe Leu
 305 310 315 320
 10 Lys Thr Lys Asn Ser Glu Ala Lys Leu Asn Val Ala Leu Ala Leu Leu
 325 330 335
 Glu Leu Gly Cys Asp Thr Pro Lys Leu Leu Glu Tyr Ile Thr Glu Arg
 340 345 350
 Leu Val Gln Pro His Tyr Asn Glu Thr Leu Ala Leu Ser Phe Ser Lys
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 20 Gly Arg Thr Leu Gln Asn Trp Lys Arg Val Asn Ile Ile Val Pro Gln
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 Asp Pro Gln Glu Arg Glu Arg Leu Leu Ser Thr Thr Arg Gly Leu Glu
 385 390 395 400
 Glu Gln Ile Leu Thr Phe Leu Phe Arg Leu Pro Lys Glu Ala Tyr Leu
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 Pro Cys Ile Tyr Lys Leu Leu Ala Ser Gln Lys Thr Gln Leu Ala Thr
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 30 Thr Ala Ile Ser Phe Leu Ser His Thr Ser His Gln Glu Ala Leu Asp
 435 440 445
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 Tyr Ala Asp Leu Ala Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys
 465 470 475 480
 40 Arg Ser Leu His Asp Tyr Ala Lys Lys Leu Ile Gln Glu Thr Leu Leu
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 Phe Val Asp Thr Glu Asn Gln Arg Pro His Pro Ser Met Pro Tyr Leu
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 50 Leu Glu Thr Leu Ala Thr Ser Lys Ser Ser Glu Asp Ile Arg Leu Leu
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